

[illegible]

Fig. 1A

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MDYGGALSAVGRELLFVTNPVVNGSVLVPEDQCYCAGWIE
SRGTNGAQTASNVLQWLAAGFSILLMFYAYQTWKSTCGWE
EIYVCAIEMVKVILEFFFEFKNPSMLYLATGHRVQWLRYAEWL
LTCPVILIHLSNLTGLSNDYSRRTMGLLVSDIGTIVWGATSAMA
TGYVKVIFFCLGLCYGANTFFHAAKAYIEGYHTVPGRCRQV
VTGMAWLFFVSWGMFPILFILGPEGFGVLSVYGSTVGHTIIDL
MSKNCWGLLGHYLRVLIHEHILIHGDIRKTTKLNIGGTEIEVETL
VEDEAEAGAVNKG TGKYASRESFLVMRDKMKEKGIDVRASL
DNSKEVEQEQAARAAMMMMNNGMGMGMGMNGMNGMG
GMNGMAGGAKPGLLELTPQLQPGRVILAVPDISMVDFFREQFA
QLSVTYELVPALGADNTLALVTQAQNLGGVDFVLIHPEFLRDR
SSTSILSRLRGAGQRVAAFGWAQLGPMRDLIESANLDGWLE
GPSFGQGILPAHIVALVAKMQQMRKMQQMQQIGMMTGGMN
GMGGGMGGGMNGMGGGNGMNNMGNGMGGGMGNGMG
NGMNGMGGGNGMNNMGNGMAGNGMGGGMGGNGMG
SMNGMSSGVVANVTPSAAGGMGGMMNGGMAAPQSPGMN
GGRLGTNPLFNAAPSPLSSQLGAEAGMGSMGGMGMSGM
GGMGGMGGMGGGAGAATTQAAGGNAEAEMLQNLMEINRL
KRELGE (SEQ ID NO:2)

Fig 1B

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MlptavegvsqAQITGRPEWIWLALGTALMGLGTLYFLVKGMGVS
DPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPFGGEQNPI
YWARYADWLFTTPLL LLDLALLVDADQG TILALVGADGIMIGT
GLVGALTKVYSYRFVWWAISTAAMLYILYVLFFGFTSKAESMR
PEVASTFKVLRNVTVVLWSAYPVVWLIGSEGAGIVPLNIETLLF
MVLDVSAKVGFG LILLRSRAIFGEAEAPEPSAGDGAAATSD
(SEQ ID NO: 3)

Fig. 1C

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Chop1..MSRRPWLALALAAAGSAGASTGSDATVPVATQDGPDYVFHRAHEMI FQTSYTLEN 60
 Chop2.....MDYGGALS AVGRELLFVTNPVV 23
 Bop.....M

* *
 Chop1..NGSVICIPNNGQCECLAWLKS N--GINA EKIAANI QNITFALSA CIMEYCYOTNKSTC 118
 Chop2..NGSVL-VPED-QCYCAGWIESR- -GTNGAQOTASNVBONLAA GFS ILLIMFYAYQETKSTC 79
 Bop..LPTAVEGVSQAQITGRPRPEWIWLALGTALMG GTLYFLVKGMGVSDPDAKKEFYAI T TLVPA 51

* * * * *
 Chop1..GWEEYVATIEIMIKFIIYFHEEDEFDAVI SSNGNKTVLR AEWLLTCEPVH IHLNLE 178
 Chop2..GWEEYVCAFEVAVKVI LLEFFEFKNE SML L LATCHRVQWIRAEWLLTCEPVH IHLNLE 139
 Bop..IAFTMY---LSMLLGYGLTMVPEGGEQ-----NPIYARADMEFTTPI L D A--L 100

* * * * *
 Chop1..GLANDYNKRTM-GLIVSDICTIVWGTIAAISKGIV -EVIFFELMCLCYCIITFEENAA-KV 235
 Chop2..GLSNBYSRRTM-GLIVSDICTIVWCAISAMATGYV-KVIFFCILGICYGANTFHHAA-KAY 196
 Bop..V-DAD-Q-GTILAIVGADGIMIGTGLVGALTIVSYK FVWWAISTAAML ILYVLEFFGFT 157

Fig. 1D

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Chop1... IEAHTVPKGI CDLMRYLAWIYFCSWAMFPEVFLFGPEGCHINQFNSAIAIAAIDIA 295

Chop2... IEGMHTVPKGRCDQVATGMWIFVSWGMPFIIFIGPECHALLSVYGSTVGTIIDIMS 256

Bop... SKAESMRPEV--ASTFKVIRNVTVVLLWSAYPVVWIISEGACIVPLNIEITLLFMVDSA 215

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Chop1... KNAMSMMGHEFLRVKIHHEHLLLYGDIKPKQKVNVAQOMVEVEFMHEHDDDETQKVP-TAKY 354

Chop2... KNCWGLLGHYERVLHHEHLLIHGDIKPKTKLNIIGTIEIEVEILLDEDAEAGAVNKGUGKY 316

Bop... KVGEGLI--LIERSRAIFGEAEPEPSAGDGA-AATSD (SEQ ID No: 3)

Chop1... ANRDSKIIIMRDLKEKGFETPASLDGDPNGDAEANAAGGKPGMEMCKMTGMGM SMGAGM 414

Chop2... ASRESFLVMRDKMKKCIDVRASLNSKEVEQEQAAARAAMMMNNGMGMGMNGMNGM 376

Chop1... GMATIDS-----GRVILAVPDISMVDFFEREQFARLPVPYELVLPALGAENT 459

Chop2... GCMNGMAGGAKPGLLTPQLQPGRVILAVPDISMVDFFEREQFAQLSVHYELVLPALGADNT 436

Chop1... IOIMQQAQSLGGCDEVMHPEFLPDRSPITGLIPRIKMGQRAAFAFGWAAIIGPMRDLIEGS 519

Chop2... EALYTQAQNLGGVDEVLIHPEFLPDRSSTISIRLRGAGQVVAAPFGWAQLGPMRDLIEISA 496

Chop1... GVDGNLEGPSFGAGINQQALVALINRMQQAKRMGMG-----GMGMGMGGGMGMG-N 568

Chop2... NLDGNLEGPSFGQGILPAHIVALVAKMQQMRPMQQMQQIGMMTGGMNCGMGGMGGGMNGM 556

Fig. 1D (continued)

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Chop1..CMCMCMG--MAPS--NAGTGGNCG---ASNGG-----AVMCMGCMQPIQQAMP--AMSPM 616

Chop2..GGNGMNNNMGNGMGCGNCGMNGCGGCGNGMNNMCGNAGNGMGGG--GGNGMGGS 616

| | Chop1.. | Chop2.. |
|--------|---|-------------------------|
| MTQQPS | -MMSQPSAMSAGGAMQAMGGVMPSPAP---- | GGPVGTNPLEGGAPSPSSQ---- |
| MNGMS | GVVANVTPSAAGGMGGMNNGGMAAPQSPGMNGGRLGTNPPLTNAPSPSSQLGA | 667 |
| | | 676 |

(Seq ID N0:1) Chop1. .-----PGISPGMATPPAATAAPACGSEAEMQQLMSEINPIN-ELGEEK 712

(Seq ID N0:2) Chop2. .EAGMGSMGGMGSMGGMGGMGGAGATQAGCNAEAEMQNLMNEINPIKRELGE 737

Fig. 1D (continued)

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....5...10....5...20....5...30....5...40

| | |
|---|-----|
| MDYGGALSAVGRELLFVTNPVVVNGSVLVPEDQCYCAGWI | 40 |
| ESRGTNGAQTASNVLQWLAAGFSILLMFYAYQTWKSTCG | 80 |
| WEEIYVCAIEMVKVILEFFFFEFKNPSMLYLATGHRVQWLR | 120 |
| YAEWLLTCPVILIRLSNLTGLSNDYSRRTMGLLVSDIGTI | 160 |
| VWGATSAMATGYVKVIFFCGLGLCYGANTFFHAAKAYIEGY | 200 |
| HTVPKGRCRQVVTGMAWLFFVSWGMEPILFILGPEGFGVL | 240 |
| SVYGSTVGHTIIDLMSKNCWGLLGHYLRVLIHEHILIHGD | 280 |
| IRKTTKLNIGGTEIEVETLVEDEAEAGAVNKGTGK (<u>SEQ ID NO. 4</u>) | 315 |

Fig. 1E